

SEQUENCE LISTING

Sub
a1

<110> Abbott Laboratories
Mukerji, Pradip
Huang, Yung-Sheng
Das, Tapas
Thurmond, Jennifer M.
Pereira, Suzette L.

<120> DESATURASE GENES AND USES THEREOF

<130> 6763.US.P1

<140> Not Yet Assigned
<141> 2002-01-22

<150> US 09/769,863
<151> 2001-01-25

<160> 55

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<222> (3)...(3)
<223> b = g or c or t/u at position 3

<221> misc_feature
<222> (6)...(6)
<223> y = t/u or c at position 6

<221> misc_feature
<222> (9)...(9)
<223> y = t/u or c at position 9

<221> misc_feature
<222> (12)...(12)
<223> b = g or c or t/u at position 12

<221> misc_difference
<222> (18)...(18)
<223> r = g or a at position 18

<221> misc_feature
<222> (24)...(24)
<223> b = g or c or t/u at position 24

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<221> misc_feature
 <222> (30)...(30)
 <223> b = g or c or t/u at position 30

<221> misc_feature
 <222> (33)...(33)
 <223> y = t/u or c at position 33

<221> misc_feature
 <222> (36)...(36)
 <223> y = t/u or c at position 36

<221> misc_feature
 <222> (39)...(39)
 <223> h = a or c or t/u at position 39

<221> misc_feature
 <222> (42)...(42)
 <223> h = a or c or t/u at position 42

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42

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<221> misc_feature
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 <223> y = t/u or c at position 6

<221> misc_feature
 <222> (12)...(12)
 <223> y = t/u or c at position 12

<221> misc_feature
 <222> (27)...(27)
 <223> y = t/u or c at position 27

<221> misc_feature
 <222> (33)...(33)
 <223> y = tu or c at position 33

<221> misc_feature
 <222> (39)...(39)
 <223> b = g or c or t/u at position 39

<221> misc_feature
 <222> (41)...(41)

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<223> y = t/u or c at position 41

<221> misc_feature

<222> (45)...(45)

<223> y = t/u or c at position 45

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45

<210> 3

<211> 45

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<223> Reverse Primer R0836

<221> misc_feature

<222> (1)...(1)

<223> r = g or a at position 1

<221> misc_feature

<222> (4)...(4)

<223> r = g or a at position 4

<221> misc_feature

<222> (7)...(7)

<223> v = a or g or c at position 7

<221> misc_feature

<222> (13)...(13)

<223> r = g or a at position 13

<221> misc_feature

<222> (19)...(19)

<223> r = g or a at position 19

<221> misc_feature

<222> (34)...(34)

<223> r = g or a at position 34

<221> misc_feature

<222> (40)...(40)

<223> r = g or a at position 40

<221> misc_feature

<222> (43)...(43)

<223> d = a or g or t/u at position 43

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rtgrtgvacg ttrtgctgrt gcttccacca gtrrgcggar gdcac

45

<210> 4

<211> 36

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<220>
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 <221> misc_feature
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 <221> misc_feature
 <222> (12)...(12)
 <223> r = g or a at position 12

 <221> misc_feature
 <222> (15)...(15)
 <223> y = t/u or c at position 15

 <221> misc_feature
 <222> (18)...(18)
 <223> r = g or a at position 18

 <221> misc_feature
 <222> (21)...(21)
 <223> r = g or a at position 21

 <221> misc_feature
 <222> (24)...(24)
 <223> s = g or c at position 24

 <221> misc_feature
 <222> (27)...(27)
 <223> r = g or a at position 27

 <221> misc_feature
 <222> (30)...(30)
 <223> v = a or g or c at position 30

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36

<210> 5
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 <223> Primer R0753

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 <223> n = a or g or c or t/u, unknown, or other at
 position 10

 <221> misc_feature
 <222> (13)...(13)
 <223> r = g or a at position 13

 <221> misc_feature
 <222> (16)...(16)

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<223> n = a or g or c or t/u, unknown, or other at
position 16

<221> misc_feature

<222> (18)...(19)

<223> r = g or a at positions 18-19

<221> misc_feature

<222> (22)...(22)

<223> r = g or a at position 22

<400> 5

catcatcatn gggaanarrt grtg

24

<210> 6

<211> 30

<212> DNA

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<223> Primer RO754

<221> misc_feature

<222> (15)...(15)

<223> y = t/u or c at position 15

<221> misc_feature

<222> (18)...(18)

<223> y = t/u or c at position 19

<221> misc_feature

<222> (21)...(21)

<223> n = a or g or c or t/u, unknown, or other at
position 21

<221> misc_feature

<222> (24)...(24)

<223> y = t/u or c at position 24

<221> misc_feature

<222> (27)...(27)

<223> n = a or g or c or t/u, unknown, or other at
position 27

<221> misc_feature

<222> (30)...(30)

<223> y = t/u or c at position 30

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ctactactac tacaycayac ntayacnaay

30

<210> 7

<211> 29

<212> DNA

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<223> Primer R0923

<400> 7

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29

<210> 8

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Primer R0899

<400> 8

agcggataac aatttcacac aggaaacagc

30

<210> 9

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer R0939

<400> 9

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<210> 10

<211> 31

<212> DNA

<213> Artificial Sequence

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<223> Primer R0898

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31

<210> 11

<211> 45

<212> DNA

<213> Artificial Sequence

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<223> Primer R0951

<400> 11

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45

<210> 12

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer R0960

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47

<210> 13
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 <213> Saprolegnia diclina

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 caccggggcg gcgtcgatcat gttcacgcag gccggcgaag acgcgaccga tgcgttcgct 180
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<210> 14
 <211> 453
 <212> PRT
 <213> Saprolegnia diclina

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 Tyr Asp Ile Ser Ala Phe Glu Asp His Pro Gly Gly Val Val Met Phe
 35 40 45
 Thr Gln Ala Gly Glu Asp Ala Thr Asp Ala Phe Ala Val Phe His Pro
 50 55 60
 Ser Ser Ala Leu Lys Leu Leu Glu Gln Tyr Tyr Val Gly Asp Val Asp
 65 70 75 80
 Gln Ser Thr Ala Ala Val Asp Thr Ser Ile Ser Asp Glu Val Lys Lys
 85 90 95
 Ser Gln Ser Asp Phe Ile Ala Ser Tyr Arg Lys Leu Arg Leu Glu Val
 100 105 110
 Lys Arg Leu Gly Leu Tyr Asp Ser Ser Lys Leu Tyr Tyr Leu Tyr Lys
 115 120 125
 Cys Ala Ser Thr Leu Ser Ile Ala Leu Val Ser Ala Ala Ile Cys Leu
 130 135 140

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His Phe Asp Ser Thr Ala Met Tyr Met Val Ala Ala Val Ile Leu Gly
 145 150 155 160
 Leu Phe Tyr Gln Gln Cys Gly Trp Leu Ala His Asp Phe Leu His His
 165 170 175
 Gln Val Phe Glu Asn His Leu Phe Gly Asp Leu Val Gly Val Met Val
 180 185 190
 Gly Asn Leu Trp Gln Gly Phe Ser Val Gln Trp Trp Lys Asn Lys His
 195 200 205
 Asn Thr His His Ala Ile Pro Asn Leu His Ala Thr Pro Glu Ile Ala
 210 215 220
 Phe His Gly Asp Pro Asp Ile Asp Thr Met Pro Ile Leu Ala Trp Ser
 225 230 235 240
 Leu Lys Met Ala Gln His Ala Val Asp Ser Pro Val Gly Leu Phe Phe
 245 250 255
 Met Arg Tyr Gln Ala Tyr Leu Tyr Phe Pro Ile Leu Leu Phe Ala Arg
 260 265 270
 Ile Ser Trp Val Ile Gln Ser Ala Met Tyr Ala Phe Tyr Asn Val Gly
 275 280 285
 Pro Gly Gly Thr Phe Asp Lys Val Gln Tyr Pro Leu Leu Glu Arg Ala
 290 295 300
 Gly Leu Leu Leu Tyr Tyr Gly Trp Asn Leu Gly Leu Val Tyr Ala Ala
 305 310 315 320
 Asn Met Ser Leu Leu Gln Ala Ala Ala Phe Leu Phe Val Ser Gln Ala
 325 330 335
 Ser Cys Gly Leu Phe Leu Ala Met Val Phe Ser Val Gly His Asn Gly
 340 345 350
 Met Glu Val Phe Asp Lys Asp Ser Lys Pro Asp Phe Trp Lys Leu Gln
 355 360 365
 Val Leu Ser Thr Arg Asn Val Thr Ser Ser Leu Trp Ile Asp Trp Phe
 370 375 380
 Met Gly Gly Leu Asn Tyr Gln Ile Asp His His Leu Phe Pro Met Val
 385 390 395 400
 Pro Arg His Asn Leu Pro Ala Leu Asn Val Leu Val Lys Ser Leu Cys
 405 410 415
 Lys Gln Tyr Asp Ile Pro Tyr His Glu Thr Gly Phe Ile Ala Gly Met
 420 425 430
 Ala Glu Val Val Val His Leu Glu Arg Ile Ser Ile Glu Phe Phe Lys
 435 440 445
 Glu Phe Pro Ala Met
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<210> 15
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 <223> Primer R0851

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<210> 16
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Primer R0941

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gctgaacggg tggtacgagt cgaacgtg

28

<210> 17

<211> 42

<212> DNA

<213> Artificial Sequence

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<223> Primer R0953

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42

<210> 18

<211> 46

<212> DNA

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<223> Primer R0956

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46

<210> 19

<211> 1413

<212> DNA

<213> Saprolegnia diclina

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ttgccggact ttacggcggc gttcgttgcc cacttgaagc acctccgcaa catggggccag 1380
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<212> PRT

<213> Saprolegnia diclina

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Phe	Tyr	Lys	Glu	Cys	Arg	Lys	Arg	Val	Gly	Glu	Tyr	Phe	Lys	Lys	Asn
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Ile	Phe	Ala	Leu	Gln	Leu	Ala	Ala	Ala	Ala	Leu	Phe	Gly	Val	Cys	Gln
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Gly	His	His	Ile	Tyr	Thr	Asn	Val	Ala	Gly	Ser	Asp	Pro	Asp	Leu	Pro
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Val	Asn	Met	Asp	Gly	Asp	Ile	Arg	Arg	Ile	Val	Asn	Arg	Gln	Val	Phe
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			260					265					270		
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Tyr	Leu	Pro	Leu	Ala	Val	Leu	Gln	Met	Pro	Ile	Lys	Thr	Tyr	Leu	Ala
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Ile	Phe	Phe	Leu	Ala	Glu	Phe	Val	Thr	Gly	Trp	Tyr	Leu	Ala	Phe	Asn
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Phe	Gln	Val	Ser	His	Val	Ser	Thr	Glu	Cys	Gly	Tyr	Pro	Cys	Gly	Asp
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Glu	Ala	Lys	Met	Ala	Leu	Gln	Asp	Glu	Trp	Ala	Val	Ser	Gln	Val	Lys
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Thr Ser Val Asp Tyr Ala His Gly Ser Trp Met Thr Thr Phe Leu Ala
 385 390 395 400
 Gly Ala Leu Asn Tyr Gln Val Val His His Leu Phe Pro Ser Val Ser
 405 410 415
 Gln Tyr His Tyr Pro Ala Ile Ala Pro Ile Ile Val Asp Val Cys Lys
 420 425 430
 Glu Tyr Asn Ile Lys Tyr Ala Ile Leu Pro Asp Phe Thr Ala Ala Phe
 435 440 445
 Val Ala His Leu Lys His Leu Arg Asn Met Gly Gln Gln Gly Ile Ala
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 Ala Thr Ile His Met Gly
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<210> 21
 <211> 914
 <212> DNA
 <213> Homo sapiens

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 <212> DNA
 <213> Mortierella alpina

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12/24

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<400> 27
cttataactcg agtaaattggc tcgcgaggcg aagcgagtgg c 41

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<210> 28
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 <212> DNA
 <213> Thraustochytrium aureum

<400> 28
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 ggcggggtcga tcatcaagtt tctcacgacc gacggcaccg aggctgtgga cgcgacgaac 180
 gcgttttcgcg agttttcactg ccggtcgggc aaggcggaaa agtacctcaa gagcctgccc 240
 aagctcggcg cgccgagcaa gatgaagttt gacgccaagg agcaggcccg gcgcgacgcg 300
 atcacgcgag actacgtcaa gctgcgcgag gagatggtgg ccgagggcct cttcaagccc 360
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 <213> Thraustochytrium aureum

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 20 25 30
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 35 40 45
 Thr Thr Asp Gly Thr Glu Ala Val Asp Ala Thr Asn Ala Phe Arg Glu
 50 55 60
 Phe His Cys Arg Ser Gly Lys Ala Glu Lys Tyr Leu Lys Ser Leu Pro
 65 70 75 80
 Lys Leu Gly Ala Pro Ser Lys Met Lys Phe Asp Ala Lys Glu Gln Ala
 85 90 95
 Arg Arg Asp Ala Ile Thr Arg Asp Tyr Val Lys Leu Arg Glu Glu Met
 100 105 110
 Val Ala Glu Gly Leu Phe Lys Pro Ala Pro Leu His Ile Val Tyr Arg
 115 120 125
 Phe Ala Glu Ile Ala Ala Leu Phe Ala Ala Ser Phe Tyr Leu Phe Ser
 130 135 140
 Met Arg Gly Asn Val Phe Ala Thr Leu Ala Ala Ile Ala Val Gly Gly
 145 150 155 160

Ile Ala Gln Gly Arg Cys Gly Trp Leu Met His Glu Cys Gly His Phe
 165 170 175
 Ser Met Thr Gly Tyr Ile Pro Leu Asp Val Arg Leu Gln Glu Leu Val
 180 185 190
 Tyr Gly Val Gly Cys Ser Met Ser Ala Ser Trp Trp Arg Val Gln His
 195 200 205
 Asn Lys His His Ala Thr Pro Gln Lys Leu Lys His Asp Val Asp Leu
 210 215 220
 Asp Thr Leu Pro Leu Val Ala Phe Asn Glu Lys Ile Ala Ala Lys Val
 225 230 235 240
 Arg Pro Gly Ser Phe Gln Ala Lys Trp Leu Ser Ala Gln Ala Tyr Ile
 245 250 255
 Phe Ala Pro Val Ser Cys Phe Leu Val Gly Leu Phe Trp Thr Leu Phe
 260 265 270
 Leu His Pro Arg His Met Pro Arg Thr Ser His Phe Ala Glu Met Ala
 275 280 285
 Ala Val Ala Val Arg Val Val Gly Trp Ala Ala Leu Met His Ser Phe
 290 295 300
 Gly Tyr Ser Gly Ser Asp Ser Phe Gly Leu Tyr Met Ala Thr Phe Gly
 305 310 315 320
 Phe Gly Cys Thr Tyr Ile Phe Thr Asn Phe Ala Val Ser His Thr His
 325 330 335
 Leu Asp Val Thr Glu Pro Asp Glu Phe Leu His Trp Val Glu Tyr Ala
 340 345 350
 Ala Leu His Thr Thr Asn Val Ser Asn Asp Ser Trp Phe Ile Thr Trp
 355 360 365
 Trp Met Ser Tyr Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Ser
 370 375 380
 Leu Pro Gln Leu Asn Ala Pro Arg Val Ala Pro Arg Val Arg Ala Leu
 385 390 395 400
 Phe Glu Lys His Gly Met Ala Tyr Asp Glu Arg Pro Tyr Leu Thr Ala
 405 410 415
 Leu Gly Asp Thr Phe Ala Asn Leu His Ala Val Gly Gln Asn Ala Gly
 420 425 430
 Gln Ala Ala Ala Lys Ala Ala
 435

<210> 30

<211> 1338

<212> DNA

<213> *Thraustochytrium aureum*

<400> 30

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gatgcaaccg	aagcgtacaa	ggagttccac	tgcagatcct	cgaaggcggt	caagtacctc	240
aactccctgc	caaagatcga	cggcccaatc	aagtacaaat	acgacgcaaa	ggagcaggct	300
cgccatgaca	aactcacgag	ggagtatgta	gctctccgcg	aacagctcgt	caaggaggga	360
tactttgacc	ccagcccgtc	ccacattatc	tacagatgcg	ccgagttggc	agccatgttc	420
gctctctcgt	tctacctttt	ctccttcaag	ggtaacgtca	tggccactat	tgctgccatc	480
gtgattgggg	ggtgcgtgca	gggtcgttgt	gggtgggtca	tgcatgaagc	tggccactac	540
agcatgaccg	gaaacatccc	tgttgacttg	cgccttcaag	agtttttgta	cgggaattggg	600
tgtggcatga	gcggggcttg	gtggagaagc	cagcacaaca	agcaccacgc	caccccccaa	660
aagctcaagc	atgacgttga	tttggaact	cttctctctg	tcgcctggaa	cgagaaaatt	720
gcccgtcgcg	tcaagccagg	tagcttccag	gcaaagtggc	ttcatctcca	gggatacatc	780

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tttgccccag tctcctgcct tctcgttggt ctcttctgga ctttgtactt gcatectcgc 840
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<210> 31

<211> 439

<212> PRT

<213> Thraustochytrium aureum

<400> 31

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Tyr Asp Ala Thr Asn Phe Arg His Pro Gly Gly Ser Ile Ile Lys Tyr
      35          40          45
Leu Cys Thr Asp Gly Lys Glu Val Val Asp Ala Thr Glu Ala Tyr Lys
      50          55          60
Glu Phe His Cys Arg Ser Ser Lys Ala Val Lys Tyr Leu Asn Ser Leu
      65          70          75          80
Pro Lys Ile Asp Gly Pro Ile Lys Tyr Lys Tyr Asp Ala Lys Glu Gln
      85          90          95
Ala Arg His Asp Lys Leu Thr Arg Glu Tyr Val Ala Leu Arg Glu Gln
      100          105          110
Leu Val Lys Glu Gly Tyr Phe Asp Pro Ser Pro Leu His Ile Ile Tyr
      115          120          125
Arg Cys Ala Glu Leu Ala Ala Met Phe Ala Leu Ser Phe Tyr Leu Phe
      130          135          140
Ser Phe Lys Gly Asn Val Met Ala Thr Ile Ala Ala Ile Val Ile Gly
      145          150          155          160
Gly Cys Val Gln Gly Arg Cys Gly Trp Leu Met His Glu Ala Gly His
      165          170          175
Tyr Ser Met Thr Gly Asn Ile Pro Val Asp Leu Arg Leu Gln Glu Phe
      180          185          190
Leu Tyr Gly Ile Gly Cys Gly Met Ser Gly Ala Trp Trp Arg Ser Gln
      195          200          205
His Asn Lys His His Ala Thr Pro Gln Lys Leu Lys His Asp Val Asp
      210          215          220
Leu Asp Thr Leu Pro Leu Val Ala Trp Asn Glu Lys Ile Ala Arg Arg
      225          230          235          240
Val Lys Pro Gly Ser Phe Gln Ala Lys Trp Leu His Leu Gln Gly Tyr
      245          250          255
Ile Phe Ala Pro Val Ser Cys Leu Leu Val Gly Leu Phe Trp Thr Leu
      260          265          270
Tyr Leu His Pro Arg His Met Ile Arg Thr Lys Arg Asn Phe Glu Ile
      275          280          285
Phe Ser Val Ala Leu Arg Tyr Val Cys Trp Phe Ser Leu Leu Leu Ser
      290          295          300
Met Gly Tyr Thr Val Gly Glu Ser Leu Gly Leu Tyr Val Leu Thr Phe
      305          310          315          320

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Gly Leu Gly Cys Thr Tyr Ile Phe Thr His Phe Ala Val Ser His Thr
 325 330 335
 His Leu Pro Val Ser Glu Glu Asp Glu Tyr Leu His Trp Val Glu Tyr
 340 345 350
 Ala Ala Leu His Thr Thr Asn Val Ala Ile Asp Ser Tyr Val Val Thr
 355 360 365
 Trp Leu Met Ser Tyr Leu Asn Phe Gln Ile Glu His His Leu Phe Pro
 370 375 380
 Cys Cys Pro Gln Phe Arg His Pro Ala Ile Ser Ser Arg Val Lys Lys
 385 390 395 400
 Leu Phe Glu Asp Asn Gly Leu Val Tyr Asp Ala Arg Ser Tyr Val Gln
 405 410 415
 Ala Leu Lys Asp Thr Phe Gly Asn Leu His Glu Val Gly Val Asn Ala
 420 425 430
 Gly Gln Ala Ala Lys Ser Glu
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<210> 32
 <211> 1381
 <212> DNA
 <213> Thraustochytrium aureum

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 cggactatct cagaaaacac cctgggtggca gcgtgatcaa gtacgggctt gccaacaccg 180
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 gccacattgt gcgcacctat ctcttccacc ttgtgaccgg ctgggagagc ctgcgtgcat 960
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 tcgtctctta ctttgaggct tggcgccctga tgctccaaaa tcttgctgac gtcggttccc 1320
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<210> 33
 <211> 456
 <212> PRT
 <213> Thraustochytrium aureum

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<210> 34

<211> 1329

<212> DNA

<213> Isochrysis galbana

<400> 34

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aagcggcacc	caggtggctc	ggtgatcaag	ttccagctgg	gcgcccagcg	gagcgacgcg	240
tacaacaact	ttcacgtccg	ctccaagaag	gcggacaaga	tgctgtattc	gctcccgtcc	300
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gggcttggct	gcggcatgtc	gggctgctac	tggcgcaacc	agcacaacaa	gcaccacgcc	660
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ttttacgtgg	ccgtgggcgg	cacctacatc	ttcaccaact	tgcgcgtctc	gcacaccac	1020
aaggacgtcg	tcccgcacc	caagcacatc	tcgtgggcac	tctactcggc	caaccacacg	1080
accaactgct	ccgactcgcc	ctttgtcaac	tggtgggatg	cctacctcaa	cttccagatc	1140
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cgccgcgtct	tcgagaagca	cggggctcgag	tatgacgtcc	ggccatacct	ggagtgtttt	1260
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<210> 35

<211> 442

<212> PRT

<213> Isochrysis galbana

<400> 35

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Ala	Ala	Asp	Val	Thr	Val	Ser	Ser	Ile	Asp	Ala	Glu	Lys	Glu	Met	Ile
		35					40					45			
Ile	Asn	Gly	Arg	Val	Tyr	Asp	Val	Ser	Ser	Phe	Val	Lys	Arg	His	Pro
	50					55					60				
Gly	Gly	Ser	Val	Ile	Lys	Phe	Gln	Leu	Gly	Ala	Asp	Ala	Ser	Asp	Ala
65					70					75				80	
Tyr	Asn	Asn	Phe	His	Val	Arg	Ser	Lys	Lys	Ala	Asp	Lys	Met	Leu	Tyr
			85						90					95	
Ser	Leu	Pro	Ser	Arg	Pro	Ala	Glu	Ala	Gly	Tyr	Ala	Gln	Asp	Asp	Ile
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Ser	Arg	Asp	Phe	Glu	Lys	Leu	Arg	Leu	Glu	Leu	Lys	Glu	Glu	Gly	Tyr
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Phe	Glu	Pro	Asn	Leu	Val	His	Val	Ser	Tyr	Arg	Cys	Val	Glu	Val	Leu
	130					135					140				
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145					150					155					160
Leu	Gly	Ala	Ile	Val	Ala	Gly	Ile	Ala	Gln	Gly	Arg	Cys	Gly	Trp	Leu
			165					170						175	

Gln His Glu Gly Gly His Tyr Ser Leu Thr Gly Asn Ile Lys Ile Asp
 180 185 190
 Arg His Leu Gln Met Ala Ile Tyr Gly Leu Gly Cys Gly Met Ser Gly
 195 200 205
 Cys Tyr Trp Arg Asn Gln His Asn Lys His His Ala Thr Pro Gln Lys
 210 215 220
 Leu Gly Thr Asp Pro Asp Leu Gln Thr Met Pro Leu Val Ala Phe His
 225 230 235 240
 Lys Ile Val Gly Ala Lys Ala Arg Gly Lys Gly Lys Ala Trp Leu Ala
 245 250 255
 Trp Gln Ala Pro Leu Phe Phe Gly Gly Ile Ile Cys Ser Leu Val Ser
 260 265 270
 Phe Gly Trp Gln Phe Val Leu His Pro Asn His Ala Leu Arg Val His
 275 280 285
 Asn His Leu Glu Leu Ala Tyr Met Gly Leu Arg Tyr Val Leu Trp His
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 Phe Tyr Val Ala Val Gly Gly Thr Tyr Ile Phe Thr Asn Phe Ala Val
 325 330 335
 Ser His Thr His Lys Asp Val Val Pro Pro Thr Lys His Ile Ser Trp
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 Ala Leu Tyr Ser Ala Asn His Thr Thr Asn Cys Ser Asp Ser Pro Phe
 355 360 365
 Val Asn Trp Trp Met Ala Tyr Leu Asn Phe Gln Ile Glu His His Leu
 370 375 380
 Phe Pro Ser Met Pro Gln Tyr Asn His Pro Lys Ile Ala Pro Arg Val
 385 390 395 400
 Arg Ala Leu Phe Glu Lys His Gly Val Glu Tyr Asp Val Arg Pro Tyr
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 Leu Glu Cys Phe Arg Val Thr Tyr Val Asn Leu Leu Ala Val Gly Asn
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<211> 36

<212> DNA

<213> Artificial Sequence

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<223> Primer R0838

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<223> v = a or g or c at position 7

<221> misc_feature

<222> (10)...(10)

<223> r = g or a at position 10

<221> misc_feature

<222> (13)...(13)

<223> s = g or c at position 13

<221> misc_feature

<222> (16)...(16)

<223> r = g or a at position 16

<221> misc_feature

<222> (19)...(19)

<223> r = g or a at position 19

<221> misc_feature

<222> (22)...(22)

<223> y = t/u or c at position 22

<221> misc_feature

<222> (25)...(25)

<223> r = g or a at position 25

<221> misc_feature

<222> (31)...(31)

<223> r = g or a at position 31

<400> 36

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36

<210> 37

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer R01065

<400> 37

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25

<210> 38

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer R01064

<400> 38

cgccttcaag agtttttgta cggaattggg

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<210> 39

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer R01097

<400> 39

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<213> Artificial Sequence

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<223> Primer R01107

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<223> Primer R01235

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<210> 44

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<212> DNA

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<400> 44

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27

<210> 45

<211> 23

<212> DNA

<213> Artificial Sequence

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<220>
<223> Primer

<400> 45
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23

<210> 46
<211> 25
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<220>
<223> GeneRacer 3 Prime Primer

<400> 46
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25

<210> 47
<211> 26
<212> DNA
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<220>
<223> Nested Primer R01234

<400> 47
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26

<210> 48
<211> 27
<212> DNA
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<220>
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<400> 48
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27

<210> 49
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Nested 5 Prime Primer

<400> 49
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26

<210> 50
<211> 23
<212> DNA
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<220>
<223> Nested 3 Prime Primer

<400> 50
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23

<210> 51
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<212> DNA
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<220>
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